

Sequence Listing

Lasky, Laurence A.
Dowbenko, Donald J.

<120> Tyrosine Phosphorylated Cleavage Furrow-Associated
Proteins (PSTPIPs)

<130> 39766-0061CP2

<140> US 09/068,377

<141> 1998-05-08

<150> PCT/US98/01774

<151> 1998-01-30

<150> US 08/938,830

<151> 1997-09-29

<150> US 08/798,419

<151> 1997-02-07

<160> 76

<210> 1

<211> 415

<212> PRT

<213> Mus Musculus

<400> 1

Met	Met	Ala	Gln	Leu	Gln	Phe	Arg	Asp	Ala	Phe	Trp	Cys	Arg	Asp
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Phe	Thr	Ala	His	Thr	Gly	Tyr	Glu	Val	Leu	Leu	Gln	Arg	Leu	Leu
				20					25					30

Asp	Gly	Arg	Lys	Met	Cys	Lys	Asp	Val	Glu	Glu	Leu	Leu	Arg	Gln
				35					40					45

Arg	Ala	Gln	Ala	Glu	Glu	Arg	Tyr	Gly	Lys	Glu	Leu	Val	Gln	Ile
				50					55					60

Ala	Arg	Lys	Ala	Gly	Gly	Gln	Thr	Glu	Met	Asn	Ser	Leu	Arg	Thr
				65					70					75

Ser	Phe	Asp	Ser	Leu	Lys	Gln	Gln	Thr	Glu	Asn	Val	Gly	Ser	Ala
				80					85					90

His	Ile	Gln	Leu	Ala	Leu	Ala	Leu	Arg	Glu	Glu	Leu	Arg	Ser	Leu
				95					100					105

Glu	Glu	Phe	Arg	Glu	Arg	Gln	Lys	Glu	Gln	Arg	Lys	Lys	Tyr	Glu
				110					115					120

Ala	Ile	Met	Asp	Arg	Val	Gln	Lys	Ser	Lys	Leu	Ser	Leu	Tyr	Lys
				125					130					135

Lys	Thr	Met	Glu	Ser	Lys	Lys	Ala	Tyr	Asp	Gln	Lys	Cys	Arg	Asp
				140					145					150

Ala	Asp	Asp	Ala	Glu	Gln	Ala	Phe	Glu	Arg	Val	Ser	Ala	Asn	Gly
				155					160					165
His	Gln	Lys	Gln	Val	Glu	Lys	Ser	Gln	Asn	Lys	Ala	Lys	Gln	Cys
				170					175					180
Lys	Glu	Ser	Ala	Thr	Glu	Ala	Glu	Arg	Val	Tyr	Arg	Gln	Asn	Ile
				185					190					195
Glu	Gln	Leu	Glu	Arg	Ala	Arg	Thr	Glu	Trp	Glu	Gln	Glu	His	Arg
				200					205					210
Thr	Thr	Cys	Glu	Ala	Phe	Gln	Leu	Gln	Glu	Phe	Asp	Arg	Leu	Thr
				215					220					225
Ile	Leu	Arg	Asn	Ala	Leu	Trp	Val	His	Cys	Asn	Gln	Leu	Ser	Met
				230					235					240
Gln	Cys	Val	Lys	Asp	Asp	Glu	Leu	Tyr	Glu	Glu	Val	Arg	Leu	Thr
				245					250					255
Leu	Glu	Gly	Cys	Asp	Val	Glu	Gly	Asp	Ile	Asn	Gly	Phe	Ile	Gln
				260					265					270
Ser	Lys	Ser	Thr	Gly	Arg	Glu	Pro	Pro	Ala	Pro	Val	Pro	Tyr	Gln
				275					280					285
Asn	Tyr	Tyr	Asp	Arg	Glu	Val	Thr	Pro	Leu	Ile	Gly	Ser	Pro	Ser
				290					295					300
Ile	Gln	Pro	Ser	Cys	Gly	Val	Ile	Lys	Arg	Phe	Ser	Gly	Leu	Leu
				305					310					315
His	Gly	Ser	Pro	Lys	Thr	Thr	Pro	Ser	Ala	Pro	Ala	Ala	Ser	Thr
				320					325					330
Glu	Thr	Leu	Thr	Pro	Thr	Pro	Glu	Arg	Asn	Glu	Leu	Val	Tyr	Ala
				335					340					345
Ser	Ile	Glu	Val	Gln	Ala	Thr	Gln	Gly	Asn	Leu	Asn	Ser	Ser	Ala
				350					355					360
Gln	Asp	Tyr	Arg	Ala	Leu	Tyr	Asp	Tyr	Thr	Ala	Gln	Asn	Ser	Asp
				365					370					375
Glu	Leu	Asp	Ile	Ser	Ala	Gly	Asp	Ile	Leu	Ala	Val	Ile	Leu	Glu
				380					385					390
Gly	Glu	Asp	Gly	Trp	Trp	Thr	Val	Glu	Arg	Asn	Gly	Gln	Arg	Gly
				395					400					405
Phe	Val	Pro	Gly	Ser	Tyr	Leu	Glu	Lys	Leu					
				410					415					

<210> 2

<211> 2100

<212> DNA

<213> Mus Musculus

<400> 2

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agaagaagcg gaaggtctcg agcggcgcca attttaataca aagtgggaat 100

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 gaacctcata acaactcaaa caaattctca agcgctttca caaccaattg 200
 cctcctctaa cgttcatgat aacttcatga ataatgaaat cacggctagt 250
 aaaattgatg atggtaataa ttcaaaacca ctgtcacctg gttggacgga 300
 ccaaactgcg tataacgcgt ttggaatcac tacagggatg ttttaatacca 350
 ctacaatgga tgatgtatat aactatctat tcgatgatga agatacccca 400
 ccaaacccaa aaaaagaggg tgggtcgacc cacgcgtccg gtccttcct 450
 catttcgctg ctgattctag ccccaaacia aacagggtga gcctttttcc 500
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 caagaaggca tatgaccaga agtgcaggga tgcagatgat gctgagcagg 1150
 ccttcgagcg tgtgagtgcc aatggccacc agaagcaagt agaaaagagc 1200
 cagaacaaag ccaagcagtg caaggagtca gccacagagg cagaaagagt 1250
 gtacaggcaa aatatcgaac aactggagag agcgaggacc gagtgggagc 1300
 aggagcaccg gactacctgt gaggccttcc agttgcagga gtttgaccgg 1350
 ctcaccatcc tccgcaatgc cctgtgggtg cactgtaacc agctctccat 1400
 gcagtgtgtc aaggatgatg agctctatga ggaagtgcgg ctgacccttg 1450
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 actggcagag agccccagc tccggtgcct tatcagaact actatgacag 1550
 ggaggtgacc ccaactgattg gcagccctag catccagccc tcctgcggtg 1600
 tgataaagag gttctctggg ctgctacatg gaagtcccaa gaccacacct 1650

tctgctcctg ctgcttccac agagactctg actcccaccc ctgagcggaa 1700
 tgagttgggtc tacgcatcca tcgaagtgca ggcgaccag ggaaacctta 1750
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 tctgatgagc tggacatttc cgcgggagac atcctggcgg tcacacctga 1850
 aggggaggat ggctgggtga ctgtggagcg gaacggacaa cgtggctttg 1900
 tccctgggtc gtacttggag aagctctgag gaaaggctag cagtctccac 1950
 atacctccgc cctgactgtg aggtcaggac tgtttctttc catcaccgcc 2000
 caggcctcac ggggccagaa ccaagcccgg tgggtgctggg catgggctgg 2050
 gtgctggcta ctctcaataa atgtctcca gaaggaaaaa aaaaaaaaaa 2100

<210> 3
 <211> 48
 <212> PRT
 <213> Mus Musculus

<400> 3
 Leu Tyr Asp Tyr Thr Ala Gln Asn Ser Asp Glu Leu Asp Ile Ser
 1 5 10 15
 Ala Gly Asp Ile Leu Ala Val Ile Leu Glu Gly Glu Asp Gly Trp
 20 25 30
 Trp Thr Val Glu Arg Asn Gly Gln Arg Gly Phe Val Pro Gly Ser
 35 40 45
 Tyr Leu Arg

<210> 4
 <211> 50
 <212> PRT
 <213> Homo sapien

<400> 4
 Leu Tyr Gln Tyr Ile Gly Gln Asp Val Asp Glu Leu Ser Phe Asn
 1 5 10 15
 Val Asn Glu Val Ile Glu Ile Leu Ile Glu Asp Ser Ser Gly Trp
 20 25 30
 Trp Lys Gly Arg Leu His Gly Gln Glu Gly Leu Phe Pro Gly Asn
 35 40 45
 Tyr Val Glu Lys Ile
 50

<210> 5
 <211> 50
 <212> PRT
 <213> Homo sapien

<400> 5
 Leu Tyr Asp Tyr Gln Glu Lys Ser Pro Arg Glu Val Thr Met Lys
 1 5 10 15

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Lys Gly Asp Ile Leu Thr Leu Leu Asn Ser Thr Asn Lys Asp Trp
20 25 30

Trp Lys Val Glu Val Asn Asp Arg Gln Gly Phe Val Pro Ala Ala
35 40 45

Tyr Val Lys Lys Leu
50

<210> 6
<211> 50
<212> PRT
<213> Homo sapien

<400> 6
Leu Tyr Asp Tyr Gln Gly Glu Gly Ser Asp Glu Leu Ser Phe Asp
1 5 10 15

Pro Asp Asp Ile Ile Thr Asp Ile Glu Met Val Asp Glu Gly Trp
20 25 30

Trp Arg Gly Gln Cys Arg Gly His Phe Gly Leu Phe Pro Ala Asn
35 40 45

Tyr Val Lys Leu Leu
50

<210> 7
<211> 48
<212> PRT
<213> Homo sapien

<400> 7
Leu Tyr Asp Tyr Gln Ala Ala Gly Asp Asp Glu Ile Ser Phe Asp
1 5 10 15

Pro Asp Asp Ile Ile Thr Asn Ile Glu Met Ile Asp Asp Gly Trp
20 25 30

Trp Arg Gly Val Cys Lys Gly Arg Tyr Gly Leu Phe Pro Ala Asn
35 40 45

Tyr val Glu

<210> 8
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid epitope tag

<400> 8
Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

<210> 9
<211> 33
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 9
cgcggatcca ccatgatggc ccagctgcag ttc 33

<210> 10

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 10
gtacgcgtcg actcacttgt catcgtcgtc cttgtagtcg agctt 45

<210> 11

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 11
tgcctttctc tccacagg 18

<210> 12

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 12
ctccttgagg ttctactagt gggggctggt gtcctg 36

<210> 13

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 13
gcggccgcac tagtatccag tctgtgctcc atctgttac 39

<210> 14

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 14
gcgtttggaa tcactac 17

<210> 15

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 15

ttatagttta gcggccgctc accggtagtc ctgggctgat g 41

<210> 16

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 16

gtacgcgtcg accgcactct acgactacac tgcacag 37

<210> 17

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 17

ctctggcgaa gaagtcc 17

<210> 18

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 18

gatcgaattc ccagaacctc aaggagaact gc 32

<210> 19

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 19

gatcctcgag ttacacccgt gtccactctg ctggagga 38

<210> 20

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic oligopeptide

<400> 20

Gly Phe Asn Leu Arg Ile Gly Arg Pro Lys Gly Pro Arg Asp Pro
1 5 10 15

Pro Ala Glu Trp Thr
20

<210> 21
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic oligopeptide

<400> 21
Gly Phe Gly Asn Arg Phe Ser Lys Pro Lys Gly Pro Arg Asn Pro
1 5 10 15

Pro Ser Ala Trp

<210> 22
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic oligopeptide

<400> 22
Gly Phe Gly Asn Arg Cys Gly Lys Pro Lys Gly Pro Arg Asp Pro
1 5 10 15

Pro Ser Glu Trp Thr
20

<210> 23
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic oligopeptide

<400> 23
Gly Gly Val Leu Arg Ser Ile Ser Val Pro Ala Pro Pro Thr Leu
1 5 10 15

Pro Met Ala Asp Thr
20

<210> 24
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 24
gtatatgtcc tggccagccc atggggttcc cagcag 36

<210> 25
<211> 36
<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 25

gcaggtcgac tctagattac acccgtgtcc actctg 36

<210> 26

<211> 907

<212> PRT

<213> Saccharomyces Pombe

<400> 26

Met Leu Thr Lys Ser Leu Gln Gly Ser Glu Asp Ala Gly Met Asp
1 5 10 15

Ala Leu Met Ser Arg Thr Lys Ser Ser Leu Ser Val Leu Glu Ser
20 25 30

Ile Asp Glu Phe Tyr Ala Lys Arg Ala Ser Ile Glu Arg Glu Tyr
35 40 45

Ala Ser Lys Leu Gln Glu Leu Ala Ala Ser Ser Ala Asp Ile Pro
50 55 60

Glu Val Gly Ser Thr Leu Asn Asn Ile Leu Ser Met Arg Thr Glu
65 70 75

Thr Gly Ser Met Ala Lys Ala His Glu Glu Val Ser Gln Gln Ile
80 85 90

Asn Thr Glu Leu Arg Asn Lys Ile Arg Glu Tyr Ile Asp Gln Thr
95 100 105

Glu Gln Gln Lys Val Val Ala Ala Asn Ala Ile Glu Glu Leu Tyr
110 115 120

Gln Lys Lys Thr Ala Leu Glu Ile Asp Leu Ser Glu Lys Lys Asp
125 130 135

Ala Tyr Glu Tyr Ser Cys Asn Lys Leu Asn Ser Tyr Met Arg Gln
140 145 150

Thr Lys Lys Met Thr Gly Arg Glu Leu Asp Lys Tyr Asn Leu Lys
155 160 165

Ile Arg Gln Ala Ala Leu Ala Val Lys Lys Met Asp Ala Glu Tyr
170 175 180

Arg Glu Thr Asn Glu Leu Leu Leu Thr Val Thr Arg Glu Trp Ile
185 190 195

Asp Arg Trp Thr Glu Val Cys Asp Ala Phe Gln His Ile Glu Glu
200 205 210

Tyr Arg Leu Glu Phe Leu Lys Thr Asn Met Trp Ala Tyr Ala Asn
215 220 225

Ile Ile Ser Thr Ala Cys Val Lys Asp Asp Glu Ser Cys Glu Lys
230 235 240

Ile Arg Leu Thr Leu Glu Asn Thr Asn Ile Asp Glu Asp Ile Thr

	245		250		255								
Gln Met Ile Gln	Asn 260	Glu Gly Thr Gly	Thr 265	Thr Ile Pro Pro	Leu 270								
Pro Glu Phe Asn	Asp 275	Tyr Phe Lys Glu	Asn 280	Gly Leu Asn Tyr	Asp 285								
Ile Asp Gln Leu	Ile 290	Ser Lys Ala Pro	Ser 295	Tyr Pro Tyr Ser	Ser 300								
Ser Arg Pro Ser	Ala 305	Ser Ala Ser Leu	Ala 310	Ser Ser Pro Thr	Arg 315								
Ser Ala Phe Arg	Pro 320	Lys Thr Ser Glu	Thr 325	Val Ser Ser Glu	Val 330								
Val Ser Ser Pro	Pro 335	Thr Ser Pro Leu	His 340	Ser Pro Val Lys	Pro 345								
Val Ser Asn Glu	Gln 350	Val Glu Gln Val	Thr 355	Glu Val Glu Leu	Ser 360								
Ile Pro Val Pro	Ser 365	Ile Gln Glu Ala	Glu 370	Ser Gln Lys Pro	Val 375								
Leu Thr Gly Ser	Ser 380	Met Arg Arg Pro	Ser 385	Val Thr Ser Pro	Thr 390								
Phe Glu Val Ala	Ala 395	Arg Pro Leu Thr	Ser 400	Met Asp Val Arg	Ser 405								
Ser His Asn Ala	Glu 410	Thr Glu Val Gln	Ala 415	Ile Pro Ala Ala	Thr 420								
Asp Ile Ser Pro	Glu 425	Val Lys Glu Gly	Lys 430	Asn Ser Glu Asn	Ala 435								
Ile Thr Lys Asp	Asn 440	Asp Asp Ile Ile	Leu 445	Ser Ser Gln Leu	Gln 450								
Pro Thr Ala Thr	Gly 455	Ser Arg Ser Ser	Arg 460	Leu Ser Phe Ser	Arg 465								
His Gly His Gly	Ser 470	Gln Thr Ser Leu	Gly 475	Ser Ile Lys Arg	Lys 480								
Ser Ile Met Glu	Arg 485	Met Gly Arg Pro	Thr 490	Ser Pro Phe Met	Gly 495								
Ser Ser Phe Ser	Asn 500	Met Gly Ser Arg	Ser 505	Thr Ser Pro Thr	Lys 510								
Glu Gly Phe Ala	Ser 515	Asn Gln His Ala	Thr 520	Gly Ala Ser Val	Gln 525								
Ser Asp Glu Leu	Glu 530	Asp Ile Asp Pro	Arg 535	Ala Asn Val Val	Leu 540								
Asn Val Gly Pro	Asn 545	Met Leu Ser Val	Gly 550	Glu Ala Pro Val	Glu 555								
Ser Thr Ser Lys	Glu Glu Asp Lys Asp	Val Pro Asp Pro Ile Ala											

	560		565		570
Asn Ala Met Ala	Glu 575	Leu Ser Ser Ser	Met 580	Arg Arg Arg Gln	Ser 585
Thr Ser Val Asp	Asp 590	Glu Ala Pro Val	Ser 595	Leu Ser Lys Thr	Ser 600
Ser Ser Thr Arg	Leu 605	Asn Gly Leu Gly	Tyr 610	His Ser Arg Asn	Thr 615
Ser Ile Ala Ser	Asp 620	Ile Asp Gly Val	Pro 625	Lys Lys Ser Thr	Leu 630
Gly Ala Pro Pro	Ala 635	Ala His Thr Ser	Ala 640	Gln Met Gln Arg	Met 645
Ser Asn Ser Phe	Ala 650	Ser Gln Thr Lys	Gln 655	Val Phe Gly Glu	Gln 660
Arg Thr Glu Asn	Ser 665	Ala Arg Glu Ser	Leu 670	Arg His Ser Arg	Ser 675
Asn Met Ser Arg	Ser 680	Pro Ser Pro Met	Leu 685	Ser Arg Arg Ser	Ser 690
Thr Leu Arg Pro	Ser 695	Phe Glu Arg Ser	Ala 700	Ser Ser Leu Ser	Val 705
Arg Gln Ser Asp	Val 710	Val Ser Pro Ala	Pro 715	Ser Thr Arg Ala	Arg 720
Gly Gln Ser Val	Ser 725	Gly Gln Gln Arg	Pro 730	Ser Ser Ser Met	Ser 735
Leu Tyr Gly Glu	Tyr 740	Asn Lys Ser Gln	Pro 745	Gln Leu Ser Met	Gln 750
Arg Ser Val Ser	Pro 755	Asn Pro Leu Gly	Pro 760	Asn Arg Arg Ser	Ser 765
Ser Val Leu Gln	Ser 770	Gln Lys Ser Thr	Ser 775	Ser Asn Thr Ser	Asn 780
Arg Asn Asn Gly	Gly 785	Tyr Ser Gly Ser	Arg 790	Pro Ser Ser Glu	Met 795
Gly His Arg Tyr	Gly 800	Ser Met Ser Gly	Arg 805	Ser Met Arg Gln	Val 810
Ser Gln Arg Ser	Thr 815	Ser Arg Ala Arg	Ser 820	Pro Glu Pro Thr	Asn 825
Arg Asn Ser Val	Gln 830	Ser Lys Asn Val	Asp 835	Pro Arg Ala Thr	Phe 840
Thr Ala Glu Gly	Glu 845	Pro Ile Leu Gly	Tyr 850	Val Ile Ala Leu	Tyr 855
Asp Tyr Gln Ala	Gln 860	Ile Pro Glu Glu	Ile 865	Ser Phe Gln Lys	Gly 870
Asp Thr Leu Met	Val	Leu Arg Thr Gln	Glu	Asp Gly Trp Trp	Asp

875

880

885

Gly Glu Ile Ile Asn Val Pro Asn Ser Lys Arg Gly Leu Phe Pro
 890 895 900

Ser Asn Phe Val Gln Thr Val
 905

<210> 27

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> This is a consensus sequence representing yeast and mice.

<220>

<221> Variant

<222> (2)...(3)

<223> Xaa = any amino acid

<400> 27

Pro Xaa Xaa Pro

1

<210> 28

<211> 1613

<212> DNA

<213> Homo sapien

<400> 28

acgatcacta tagggcgaat tgggcctcta gatgcatgct cgagcggccg 50

ccagtgtgat ggatatctgc agaattcggc ttccatccta atacgactca 100

ctatagggct cgagcggccg cccgggcagg tctagaattc agcggccgct 150

gaattctctt tttcctcccc tcagaagctc ctctctggct cgtggctgcc 200

ttctgagtgt tgcagacggc gccggccggg aagggggggc tgggccagcc 250

ctgccaggac tgggacgctg ctgctgacgc ctggccctcc atcaggccag 300

cctgtggcag gagagtgagc tttgccgcgg cagacgcctg aggatgatgc 350

cccagctgca gttcaaagat gccttttggt gcagggactt cacagcccac 400

acgggctacg aggtgctgct gcagcggctt ctggatggca ggaagatgtg 450

caaagacatg gaggagctac tgaggcagag ggcccaggcg gaggagcggc 500

acgggaagga gctggtgcag atcgcacgga aggcaggtgg ccagacggag 550

atcaactccc tgagggcctc ctttgactcc ttgaagcagc aaatggagaa 600

tgtgggcagc tcacacatcc agctggccct gaccctgcgt gaggagctgc 650

ggagtctcga ggagtttcgt gagaggcaga aggagcagag gaagaagggc 700

atggctgtcc cgagacagag tgactgcatg gaagtgaagt ccccatcatg 750

ggagtatgag gccgtcatgg accgggtcca gaagagcaag ctgtcgctct 800

acaagaaggc catggagtcc aagaagacat acgagcagaa gtgccgggac 850
 gcggacgacg cggagcaggc cttcagcgc attagcgcca acggccacca 900
 gaagcaggtg gagaagagtc agaacaagc caggcagtgc aaggactcgg 950
 ccaccgaggc agagcgggta tacaggcaga gcattgcgca gctggagaag 1000
 gtccgggctg agtgggagca ggagcaccgg accacctgtg aggcctttca 1050
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 acagtaacca gctctccatg cagtgtgtca aggatgatga gctctacgag 1150
 gaagtgcggc tgacgctgga aggctgcagc atagacgccg acatcgacag 1200
 tttcatccag gccaagagca cgggcacaga gccccccagg ttctctggac 1250
 tgctgcacgg aagtcccaag accacttcgt cagcttctgc tggctccaca 1300
 gagaccctga cccccacccc cgagcggaat gaggggtgtct acacagccat 1350
 cgcagtgcag gagatacagg gaaaccggc ctcaccagcc caggactacc 1400
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 cgggcagcgt ggcttcgtcc ctggttccta cctggagaag ctttgaggga 1550
 aggccaggag ccccttcgga cctccgcct gccagtggag ccagcagtgc 1600
 ccccgact gtc 1613

<210> 29

<211> 400

<212> PRT

<213> Homo sapien

<400> 29

Met Met Pro Gln Leu Gln Phe Lys Asp Ala Phe Trp Cys Arg Asp
 1 5 10 15
 Phe Thr Ala His Thr Gly Tyr Glu Val Leu Leu Gln Arg Leu Leu
 20 25 30
 Asp Gly Arg Lys Met Cys Lys Asp Met Glu Glu Leu Leu Arg Gln
 35 40 45
 Arg Ala Gln Ala Glu Glu Arg Tyr Gly Lys Glu Leu Val Gln Ile
 50 55 60
 Ala Arg Lys Ala Gly Gly Gln Thr Glu Ile Asn Ser Leu Arg Ala
 65 70 75
 Ser Phe Asp Ser Leu Lys Gln Gln Met Glu Asn Val Gly Ser Ser
 80 85 90
 His Ile Gln Leu Ala Leu Thr Leu Arg Glu Glu Leu Arg Ser Leu
 95 100 105
 Glu Glu Phe Arg Glu Arg Gln Lys Glu Gln Arg Lys Lys Gly Met
 110 115 120

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Ala Val Pro Arg	Gln 125	Ser Asp Cys Met	Glu 130	Val Lys Ser Pro	Ser 135
Trp Glu Tyr Glu	Ala 140	Val Met Asp Arg	Val 145	Gln Lys Ser Lys	Leu 150
Ser Leu Tyr Lys	Lys 155	Ala Met Glu Ser	Lys 160	Lys Thr Tyr Glu	Gln 165
Lys Cys Arg Asp	Ala 170	Asp Asp Ala Glu	Gln 175	Ala Phe Glu Arg	Ile 180
Ser Ala Asn Gly	His 185	Gln Lys Gln Val	Glu 190	Lys Ser Gln Asn	Lys 195
Ala Arg Gln Cys	Lys 200	Asp Ser Ala Thr	Glu 205	Ala Glu Arg Val	Tyr 210
Arg Gln Ser Ile	Ala 215	Gln Leu Glu Lys	Val 220	Arg Ala Glu Trp	Glu 225
Gln Glu His Arg	Thr 230	Thr Cys Glu Ala	Phe 235	Gln Leu Gln Glu	Phe 240
Asp Arg Leu Thr	Ile 245	Leu Arg Asn Ala	Leu 250	Trp Val His Ser	Asn 255
Gln Leu Ser Met	Gln 260	Cys Val Lys Asp	Asp 265	Glu Leu Tyr Glu	Glu 270
Val Arg Leu Thr	Leu 275	Glu Gly Cys Ser	Ile 280	Asp Ala Asp Ile	Asp 285
Ser Phe Ile Gln	Ala 290	Lys Ser Thr Gly	Thr 295	Glu Pro Pro Arg	Phe 300
Ser Gly Leu Leu	His 305	Gly Ser Pro Lys	Thr 310	Thr Ser Ser Ala	Ser 315
Ala Gly Ser Thr	Glu 320	Thr Leu Thr Pro	Thr 325	Pro Glu Arg Asn	Glu 330
Gly Val Tyr Thr	Ala 335	Ile Ala Val Gln	Glu 340	Ile Gln Gly Asn	Pro 345
Ala Ser Pro Ala	Gln 350	Asp Tyr Arg Ala	Leu 355	Tyr Asp Tyr Thr	Ala 360
Gln Asn Pro Asp	Glu 365	Leu Asp Leu Ser	Ala 370	Gly Asp Ile Leu	Glu 375
Gly Glu Asp Gly	Trp 380	Trp Thr Val Glu	Arg 385	Asn Gly Gln Arg	Gly 390
Phe Val Pro Gly	Ser 395	Tyr Leu Glu Lys	Leu 400		

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